

RAW SEQUENCE LISTING US/09/688,459
DATE: 02/15/2001 TIME: 23:57:44
INPUT SET: S36394.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

(1) APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
(11) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappab
(111) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESS: Immunex Corporation, Law Department
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: floppy disk
(B) COMPUTER: Apple Power Macintosh
(C) OPERATING SYSTEM: Apple Operating System 7.5.5
(D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/688,459
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/995,659
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 08/813,509
(B) FILING DATE: 07 MARCH 1997
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 08/772,330
(B) FILING DATE: 23 DECEMBER 1996
(C) CLASSIFICATION:

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47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Perkins, Patricia Anne
49 (B) REGISTRATION NUMBER: 34,693
50 (C) REFERENCE/DOCKET NUMBER: 2852-A
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: (206) 587-0430
54 (B) TELEFAX: (206) 233-0644
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56
57 (2) INFORMATION FOR SEQ ID NO:1:
58
59 (1) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 3115 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: cDNA
66
67 (iii) HYPOTHETICAL: NO
68
69 (iv) ANTI-SENSE: NO
70
71 (v) ORIGINAL SOURCE:
72 (A) ORGANISM: HOMO SAPIENS
73
74 (vii) IMMEDIATE SOURCE:
75 (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
76 (B) CLONE: 9D-8A
77
78 (ix) FEATURE:
79 (A) NAME/KEY: CDS
80 (B) LOCATION: 93..1868
81
82
83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
84
85 GCTGCTGCTG CTCTGCGCGC TGCTGCGCGG GCTGCAAGTTT TATCCAGAAA GAGCTGTGTG
86
87 GACTCTCTGC CTGACCTCAG TGTCTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT
88
89 Val Ala Leu Gln Ile Ala Pro
90 1 5
91 CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC
92 Pro Cys Thr Ser Gln Lys His Tyr Gln His Leu Gln Arg Cys Cys Asn
93 10 15 20
94 AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT
95 Lys Cys Gln Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser
96 25 30 35
97
98
99 GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG
257

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100	Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Ser	Trp	55
101																	
102																	
103	AAT	GAA	GAA	GAT	AAA	TGC	TTC	CTG	CAT	AAA	GTT	TGT	GAT	ACA	GGC	AAG	305
104	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Thr	Gly	Lys	
105																	
106																	
107	GCC	CTG	GTC	GCC	GTC	GTC	GCC	GGC	AAC	AGC	ACC	CGG	CGC	TGC			353
108	Ala	Leu	Val	Ala	Val	Ala	Gly	Asn	Ser	Thr	Thr	Pro	Arg	Arg	Cys		
109																	
110																	
111	GCG	TGC	ACG	GCT	GGG	TAC	CAC	TGG	AGC	CAG	GAC	TGC	GAG	TGC	TGC	CGC	401
112	Ala	Cys	Thr	Ala	Gly	Tyr	His	Trp	Ser	Gln	Asp	Cys	Glu	Cys	Cys	Arg	
113																	
114																	
115	GCG	AAC	ACC	GAG	TGC	GCG	GCG	GCG	CTG	GCG	GCC	CAG	CCG	TTG	CAG		449
116	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Leu	Gly	Ala	Gln	His	Pro	Leu	Gln	
117																	
118																	
119	CTC	AAC	AAG	GAC	ACA	GTC	TGC	AAA	CCT	TGC	CTT	GCA	GGC	TAC	TTC	TCT	497
120	Leu	Asn	Lys	Asp	Thr	Val	Cys	Lys	Pro	Cys	Leu	Ala	Gly	Tyr	Phe	Ser	
121																	
122																	
123	GAT	GCC	TTT	TCC	TCC	ACC	GAC	AAA	TGC	AGA	CCC	TGG	ACC	AAC	TGT	ACC	545
124	Asp	Ala	Phe	Ser	Thr	Ser	Thr	Asp	Lys	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Thr
125																	
126																	
127	TTC	CTT	GGA	AAG	AGA	GTA	GAA	CAT	CAT	GCG	ACA	GAG	AAA	TCC	GAT	GCG	593
128	Phe	Leu	Gly	Lys	Arg	Val	Glu	His	His	Gly	Thr	Glu	Lys	Ser	Asp	Ala	
129																	
130																	
131	GTT	TGC	AGT	TCT	TCT	CTG	CCA	GCT	AGA	AAA	CCA	CCA	AAT	GAA	CCC	CAT	641
132	Val	Cys	Ser	Ser	Ser	Leu	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His	
133																	
134																	
135																	
136	GTT	TAC	TTG	CCC	GGT	TTA	ATA	ATT	CTG	CTT	CTC	TTC	GCG	TCT	GTG	GCC	689
137	Val	Tyr	Leu	Pro	Gly	Leu	Ile	Ile	Leu	Leu	Phe	Ala	Ser	Val	Ala		
138																	
139	CTG	GTG	GCT	GCC	ATC	ATC	TTT	GCG	GTT	TGC	TAT	AGG	AAA	GGG	AAA		737
140	Leu	Val	Ala	Ile	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	L		

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153	250	255	260
154	ACT CTG GAG GAG AAG ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA		
155	Thr Leu Gln Gln Lys Thr Phe Pro Gln Asp Met Cys Tyr Pro Asp Gln		
156		270	275
157			
158			
159	GGT GGT GTC TGT CAG GGC AGC TGT GTA GGA GGT GGT CCC TAC GCA CAA		
160	Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln		295
161		285	
162	GGC GAA GAT GCC AGG ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG		
163	Gly Gln Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Gln Ile Gln		310
164		300	
165			
166	GAA GAC AGC TTC AGA CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG		
167	Gln Asp Ser Phe Arg Gln Met Pro Thr Gln Asp Gln Tyr Met Asp Arg		325
168		315	
169			
170	CCC TCC CAG CCC ACA GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC		
171	Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Gln Pro Gly Ser		340
172		335	
173			
174	AAA TCC ACA CCT CCT TTC TCT TCT GAA CCC CTG GAG GAG AAT GAC		
175	Lys Ser Thr Pro Phe Ser Gln Pro Leu Gln Val Gly Gln Asn Asp		355
176		350	
177			
178	AGT TTA AGC CAG TGC TTC ACC GGG ACA CAG AGC ACA GTG GGT TCA GAA		
179	Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Gln		375
180		365	
181			
182	AGC TGC AAC TGC ACT GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG		
183	Ser Cys Asn Cys Thr Gln Pro Leu Cys Arg Thr Asp Thr Pro Met		390
184		380	
185			
186	TCC TCT GAA AAC TAC TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG		
187	Ser Ser Gln Asn Tyr Leu Gln Lys Gln Val Asp Ser Gly His Cys Pro		405
188		400	
189			
190	CAC TGG GCA GCC AGC CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC		
191	His Trp Ala Ala Ser Pro Asn Trp Ala Asp Val Cys Thr Gly		420
192		415	
193			
194	TGC CGG AAC CCT CCT GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA		
195	Cys Arg Asn Pro Pro Gly Gln Asp Cys Gln Pro Leu Val Gly Ser Pro		435
196		430	
197			
198	AAA CGT GGA CCC TTG CCC CAG TGC GGC TAT GGC ATG GGC CTT CCC CCT		
199	Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro		450
200		445	
201			
202	GAA GAA GAA GCC AGC AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG		
203	Gln Gln Gln Ala Ser Arg Thr Gln Ala Arg Asp Gln Pro Gln Asp Gly		465
204		460	
205			

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206 GCT GAT GGG AGG CTC CCA AGC TCA GCG AGG GCA GGT GCC GGG TCT GGA
207 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ser Gly
208 475 480 485
209
210 AGC TCC CCT GGT GGC CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC
211 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
212 490 495 500
213
214 AGT AAC TCC ACC TTC ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC
215 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
216 505 515
217
218 GAC ATC ATC GTG GTC TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG
219 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Gly Ala Ala
220 520 525 530 535
221
222 GCG GCT GCG GAG CCC ATG GGC CCG GTG CAG GAG ACG CTC GCG
223 Ala Ala Ala Gln Pro Met Gly Arg Pro Val Gln Gln Thr Leu Ala
224 540 545 550
225
226 CGC CGA GAC TCC TTC GCG GGG AAC GGC CCG GCG TTC CCG GAC CCG TGC
227 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
228 555 560 565
229
230 GGC GGC CCC GAG GGG CTG CCG GAG CCG GAG AAG GCC TCG AGG CCG GTG
231 Gly Gly Pro Gln Gly Leu Arg Gln Pro Gln Lys Ala Ser Arg Pro Val
232 570 580
233
234 CAG GAG CAA GGC GGC MAG GCT TGA GCGCCCCCA TGGCTGGAG
235 Gln Gln Gly Gly Ala Lys Ala
236 585 590
237
238
239 CCGGAAGCTC GGAGCCAGGG CTCGGCAGGG CAGCACCGCA GCCTCTGCCC CAGCCCCGGG
1948
240
241 CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCAACCCG GCATTCTCTG CCCACTTTGC
2008
242
243 CTTCCAGGAA ATGGGCTTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCACAGGA
2068
244
245 TGCTCAGCAG CCGCGCCGAC TGGGGCAGAT GTCTCCCTG CCACTCCTCA AACTCGCAGC
2128
246
247 AGTAATTGT GGCACTATGA CAGCTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGGT
2188
248
249 CTATGTTTC CCCCCTAAT TGTATTCTT TTCTAATCTT TTCTTGATAT CTTTCCCTCC
2248
250
251 TCTTTTAA TGTAAAGTT TTCTCAAAA TTCTCCTAAA GTTGAGGGTC TCTTCTTTT
2308
252
253 CTCTTTTCT TTTTCTTTC TTTTCTTGGC AACCTGGCTC TGGCCCAAGC TAGAGTGCAG
2368
254
255 TGGTGGGATT ATAGCCCGGT GCAAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGATCC
2428
256
257 TCCCACTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGGCACGGCC AGCTTCTCTC
2488
258

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/688,459

Original Text

Line
Error

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/688,459

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> > THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/688,459

DATE: 02/15/2001
TIME: 23:57:46
INPUT SET: S36394.raw

Corrected Text

Original Text

Line